WE CLAIM:

1. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence set forth in SEQ ID NO: 2 or 4;

(b) the amino sequence comprising residues 1-266 of the amino acid sequence set forth in SEQ ID NO: 2 or 4;

(c) the amino acid sequence encoded by SEQ ID NO: 1 or 3;

(d) an amino acid sequence comprising at least 50 contiguous amino acids of at least one amino acid sequence selected from the group consisting of SEQ ID NOS: 2 and 4;

(e) an amino acid sequence comprising at least 85% identity to at least one amino acid sequence selected from the group consisting of SEQ ID NOS: 2 and 4; and

(f) a fragment or variant of (a) that confers a dominant-negative phenotype in a host cell.

2. An isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence set forth in SEQ ID NO: 1 or 3;

(b) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO: 2 or 4;

(c) a nucleotide sequence encoding residues 1-266 of the amino acid sequence set forth in SEQ ID NO: 2 or 4;

(d) an antisense nucleotide sequence corresponding to the nucleotide sequence of (a), (b) or (c);

(e) a nucleotide sequence comprising at least 85% sequence identity to at least one nucleotide sequence selected from the group consisting of SEQ ID NOS:1 and 3;

(f) a nucleotide sequence comprising at least 50 contiguous nucleotides of at least one nucleotide sequence selected from the group consisting of SEQ ID NOS:1 and 3;

(g) a nucleotide sequence that hybridizes under stringent conditions to at least one nucleotide sequence selected from the group consisting of SEQ ID NOS:1 and 3; and

(h) a nucleotide sequence encoding a fragment or variant of the amino acid sequence set for in SEQ ID NO: 2 or 4, wherein said fragment or said variant confers a dominant-negative phenotype in a host cell.

3. An isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence set forth in SEQ ID NO: 5, 6, 7, 8, 9, 10, 11, or 12;

(b) a nucleotide sequence comprising at least 85% sequence identity to at least one nucleotide sequence selected from the group consisting of SEQ ID NOS:5-12;

(c) a nucleotide sequence that hybridizes under stringent conditions to at least one nucleotide sequence selected from the group consisting of SEQ ID NOS:5-12; and

(d) a nucleotide sequence comprising at least 50 contiguous nucleotides of at least one nucleotide sequence selected from the group consisting of SEQ ID NOS:5-12.

4. An expression cassette comprising a promoter operably linked to the nucleotide sequence of claim 2.

5. The expression cassette of claim 4, wherein said promoter drives expression in a plant.

6. The expression cassette of claim 5, wherein said promoter is selected from the group consisting of constitutive, pathogen-inducible, insect-inducible, wound-inducible, tissue-preferred, and developmentally regulated promoters.

7. An expression cassette comprising a first nucleotide sequence operably linked to drive the expression of a second nucleotide sequence, wherein said first nucleotide sequence is the nucleotide sequence of claim 3.

8. The expression cassette of claim 7, wherein said second sequence is a coding sequence for a protein.

9. A transformed plant comprising in its genome at least one stably incorporated nucleotide construct comprising a promoter that drives expression in a plant operably linked to the nucleotide molecule of claim 2.

10. The plant of claim 9, wherein said promoter is selected from the group consisting of constitutive, tissue-preferred and developmentally regulated promoters.

11. The plant of claim 9, wherein said plant is a monocot.

12. The plant of claim 11, wherein said monocot is selected from the group consisting of maize, wheat, rice, sorghum, barley, millet and rye.

13. The plant of claim 9, wherein said plant is a dicot.

14. The plant of claim 13, wherein said dicot is selected from the group consisting of tobacco, tomato, potato, soybean, *Brassica* sp., alfalfa, safflower, sunflower, cotton, and peanut.

15. Transformed seed of the plant of claim 9.

16. A transformed plant cell comprising in its genome at least one stably incorporated nucleotide construct comprising a promoter that drives expression in a plant cell operably linked to the nucleotide molecule of claim 2.

17. A transformed plant comprising in its genome at least one stably incorporated nucleotide construct comprising a promoter operably linked to a nucleotide sequence, wherein said promoter comprises the nucleotide molecule of claim 3.

18. A transformed plant cell comprising in its genome at least one stably incorporated nucleotide construct comprising a promoter operably linked to a nucleotide sequence, wherein said promoter comprises the nucleotide molecule of claim 3.

19. A method for altering recombination frequency in a plant comprising introducing into a plant the nucleotide molecule of claim 2, wherein the said recombination frequency is increased or decreased in said plant or at least one cell thereof.

20. The method of claim 19, wherein said nucleotide construct further comprises a promoter that drives expression in a plant cell, said promoter operably linked to said nucleotide sequence.

21. The method of claim 20, wherein said promoter is operably linked to said nucleotide sequence for the production of antisense transcripts.

22. The method of claim 20, wherein said promoter is selected from the group consisting of constitutive, tissue-preferred and developmentally regulated promoters.

23. The method of claim 19, wherein said plant or at least one cell thereof comprises a dominant negative phenotype.

24. The method of claim 19 further comprising antisense suppression or co-suppression.

25. The method of claim 19 further comprising chimeraplasty.

26. A method for altering DNA repair processes in a plant comprising introducing into a plant a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence set forth in SEQ ID NO: 1 or 3;

(b) a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO: 2 or 4;

(c) a nucleotide sequence encoding residues 1-266 of the amino acid sequence set forth in SEQ ID NO: 2 or 4;

(d) an antisense nucleotide sequence corresponding to the nucleotide sequence of (a), (b) or (c);

(e) a nucleotide sequence comprising at least 85% sequence identity to at least one nucleotide sequence selected from the group consisting of SEQ ID NOS:1 and 3;

(f) a nucleotide sequence comprising at least 50 contiguous nucleotides of at least one nucleotide sequence selected from the group consisting of SEQ ID NOS:1 and 3;

(g) a nucleotide sequence that hybridizes under stringent conditions to at least one nucleotide sequence selected from the group consisting of SEQ ID NOS:1 and 3; and

(h) a nucleotide sequence encoding a fragment or variant of the amino acid sequence set for in SEQ ID NO: 2 or 4, wherein said fragment or said variant confers a dominant-negative phenotype in a host cell;

wherein the mutation rate of at least one gene in said plant is increased or decreased.

27. The method of claim 26, wherein the efficiency of gene modification in said plant is increased.

28. The method of claim 27, wherein said gene modification comprises chimeraplasty.

29. The method of claim 26, wherein said DNA repair process comprises mismatch repair.

30. The method of claim 26 further comprising operably linking to said nucleotide sequence a promoter that drives expression in a plant cell.

31. The method of claim 30, wherein said promoter is selected from the group consisting of constitutive, tissue-preferred and developmentally regulated promoters.

32. The method of claim 26 further comprising introducing a dominant negative mutation into said nucleotide sequence.

33. The method of claim 26, wherein said plant or at least one cell thereof comprises a dominant negative phenotype.

34. The method of claim 30 further comprising antisense suppression or co-suppression.

35. The method of claim 26 further comprising chimeraplasty.

36. A non-human host cell comprising in its genome a nucleotide construct comprising the nucleotide molecule of claim 2.

37. The host cell of claim 36, wherein said nucleotide construct further comprises an operably linked promoter that is capable of driving expression of said nucleotide sequence in said host cell.